

#70m

## SEQUENCE LISTING

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<120> GENE CODING FOR HELIOMICINE, AND USE THEREOF

<130> A33595 PCT USA

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<150> PCT/FR99/00843

<151> 1999-04-12

<150> FR 98 04933

<151> 1998-04-15

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 147

<212> ADN

<213> synthetic construct

<220>

<221> CDS

<222> (1)..(147)

<400> 1

agc ttg gat aaa aga gac aag ttg att ggc agc tgt gtt tgg ggc gcc  
 48

Ser Leu Asp Lys Arg Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala  
 1 5 10 15

gtc aac tac act agt gac tgc aac ggc gag tgc aag cgc cgc ggt tac  
 96

Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr  
 20 25 30

aag ggt ggc cat tgt gga tcc ttc gct aac gtt aac tgt tgg tgt gaa  
 144

Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys Glu  
 35 40 45

acc  
147  
Thr

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<222> (1)..(132)

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gat aag ctt atc ggt tcc tgc<sup>47</sup> gtg tgg ggt gct gtg aac tac act tcc  
48  
Asp Lys Leu Ile Gly Ser Cys Val Trp Gly Ala (Val) Asn Tyr Thr Ser  
1 5 10 15

gat tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc  
96  
Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly (His) Cys  
20 25 30

ggt tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg  
142  
Gly Ser Phe Ala Asn (Val) Asn Cys Trp Cys Glu Thr  
35 40

gcgaggcgaa cgtgtcgcgc gatccgg  
169

<210> 3  
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<222> (3)..(224)

<400> 3  
cc atg ggt ttc gtg ctt ttc tct cag ctt cca tct ttc ctt ctt gtg  
47  
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val

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1               5               10               15
tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt gcc gat
95
Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Asp
                20                25                30

aag ctt atc ggt tcc tgc gtg tgg ggt gct gtg aac tac act tcc gat
143
Lys Leu Ile Gly Ser Cys Val Trp Gly Ala Val Asn Tyr Thr Ser Asp
                35                40                45

tgc aac ggt gag tgc aag agg agg ggt tac aag ggt ggt cac tgc ggt
191
Cys Asn Gly Glu Cys Lys Arg Arg Gly Tyr Lys Gly Gly His Cys Gly
                50                55                60

tcc ttc gct aac gtg aac tgc tgg tgc gag act tgagagctcg gcgaggcgaa
244
Ser Phe Ala Asn Val Asn Cys Trp Cys Glu Thr
                65                70

cgtgtcgcgacg gatccgg
261

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<210> 4
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<222> (12)..(101)

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gcgtcgacgc g atg ggt ttc gtg ctt ttc tct cag ctt cca tct ttc ctt
50
                Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu
                1                5                10

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ctt gtg tct act ctt ctt ctt ttc ctt gtg atc tct cac tct tgc cgt
98
Leu Val Ser Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg
    15                20                25

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gct ggagacgcga attcacaca
120

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Ala  
30

<210> 5  
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gcgtcgacgc gatgggtttc gtgcttttct ctcagcttcc atctttcctt cttgtgtcta  
60

ctcttcttct tttcc  
75

<210> 6  
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tcgccggcac ggcaagagta agagatcaca aggaaaagaa gaagagtaga cacaagaagg  
60

aaagatggaa gc  
72

<210> 7  
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60

gagtgcaaga ggaggggtta  
80

<210> 8  
<211> 109  
<212> ADN  
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ccggatccgt cgacacgttc gcctcgccga gctctcaagt ctgcaccag cagttcacgt  
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tagcgaagga accgcagtga ccacccttgt aaccctcct cttgcactc  
109

<210> 9  
<211> 85  
<212> ADN  
<213> synthetic construct

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agggccccct agggtttaa cggccagtca ggccgaattc gagctcggta cccggggatc  
60

ctctagagtc gacctgcagg catgc  
85

<210> 10  
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ccctgaacca ggctcgaggg cgcgccttaa ttaaagctt gcatgcctgc aggtcgactc  
60

tagagg  
66

<210> 11  
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<212> ADN  
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<400> 11  
ccggccagtc aggccacact taattaagtt taaacgcggc cccggcgcg ctaggtgtgt  
60

gctcgagggc ccaacctcag tacctgggtc agg  
93

<210> 12

<211> 93  
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 60

gcgtttaaac ttaattaagt gtggcctgac tgg  
 93

<210> 13  
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<400> 13  
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<210> 14  
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<210> 15  
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 <212> ADN  
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 <222> (7)..(72)

<400> 15  
 tctaga atg gcc tgc acc aac aac gcc atg agg gcc ctc ttc ctc ctc  
 48

Met	Ala	Cys	Thr	Asn	Asn	Ala	Met	Arg	Ala	Leu	Phe	Leu	Leu
	1			5					10				

ctg ctc ttc tgc atc gtg cac ggc gccgaattc

81  
 Leu Leu Phe Cys Ile Val His Gly  
 15 20

<210> 16  
 <211> 24  
 <212> ADN  
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<400> 16  
 gataagctta tcggttcctg cgtg  
 24

<210> 17  
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 <212> ADN  
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<400> 17  
 ggctcagagtc aagtctcgca ccagcagttc ac  
 32

<210> 18  
 <211> 213  
 <212> ADN  
 <213> synthetic construct

<220>  
 <221> CDS  
 <222> (7)..(204)

<400> 18  
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 48  
 Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu  
 1 5 10

ctg ctc ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg  
 96  
 Leu Leu Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val  
 15 20 25 30

tgg ggt gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg  
 144  
 Trp Gly Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg

35

40

45

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agg ggt tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc
192
Arg Gly Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys
      50                          55                      60
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tgg tgc gag act tgactcgag
213
Trp Cys Glu Thr
      65
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<210> 19
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<213> synthetic construct
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<220>
<221> promoter
<222> (7)..(532)
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<221> misc_structure
<222> (533)..(568)
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<220>
<221> terminator
<222> (569)..(832)
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<400> 19
aagcttccag aaggtaatta tccaagatgt agcatcaaga atccaatggt tacgggaaaa
60
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actatggaag tattatgtga gctcagcaag aagcagatca atatgcgga catatgcaac
120
```

```
ctatgttcaa aatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa
180
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gaatacgtag aaattgaaaa agaagaacca ggccaagaaa agaacttga agacgtaagc
240
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actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg
300
```

```
acacatgtaa ggtggaaaat gtaagggcgg aaagtaacct tatcacaag gaatcttatc
360
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ccccactact taccctttta tatttttccg tgtcattttt gcccttgagt tttcctatat  
420

aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgaagc tattttcttt  
480

gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctagaag  
540

gcctgaattc gagctcggta ccggatccaa ttcccgatcg ttcaaacatt tggcaataaa  
600

gtttcttaag attgaatcct gttgccggtc ttgcatgat tatcatataa tttctgttga  
660

attacgttaa gcatgtaata attaacatgt aatgcatgac gttatttatg agatggggtt  
720

ttatgattag agtcccgcaa ttatacattt aatagcgcgat agaaaacaaa atatagcgcg  
780

caaactagga taaattatcg cgcgcgggtg catctatggt actagatcgg ggatcgat  
838

<210> 20  
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<222> (7)..(532)

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<222> (539)..(736)

<220>  
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<222> (767)..(1030)

<400> 20  
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60

actatggaag tattatgtga gctcagcaag aagcagatca atatgcccga catatgcaac

120

ctatgttcaa aatgaagaa tgtacagata caagatccta tactgccaga atacgaagaa  
180

gaatacgtag aaattgaaaa agaagaacca ggcgaagaaa agaattctga agacgtaagc  
240

actgacgaca acaatgaaaa gaagaagata aggtcgggtga ttgtgaaaga gacatagagg  
300

acacatgtaa ggtggaaaat gtaagggcgg aaagtaacct tatcaciaag gaattctatc  
360

ccccactact taccctttta tatttttccg tgtcattttt gcccttgagt tttcctatat  
420

aaggaaccaa gttcggcatt tgtgaaaaca agaaaaaatt tgggtgaagc tattttcttt  
480

gaagtactga ggatacaact tcagagaaat ttgtaagttt gtagatctcg attctaga  
538

atg gcc tgc acc aac aac gcc atg agg gcc ctc ttc ctc ctc gtg ctc  
586  
Met Ala Cys Thr Asn Asn Ala Met Arg Ala Leu Phe Leu Leu Val Leu  
1 5 10 15

ttc tgc atc gtg cac ggc gat aag ctt atc ggt tcc tgc gtg tgg ggt  
634  
Phe Cys Ile Val His Gly Asp Lys Leu Ile Gly Ser Cys Val Trp Gly  
20 25 30

gct gtg aac tac act tcc gat tgc aac ggt gag tgc aag agg agg ggt  
682  
Ala Val Asn Tyr Thr Ser Asp Cys Asn Gly Glu Cys Lys Arg Arg Gly  
35 40 45

tac aag ggt ggt cac tgc ggt tcc ttc gct aac gtg aac tgc tgg tgc  
730  
Tyr Lys Gly Gly His Cys Gly Ser Phe Ala Asn Val Asn Cys Trp Cys  
50 55 60

gag act tgactcgagg gggggcccgg taccggatcc aattcccgat cgttcaaaca  
786  
Glu Thr  
65

tttggcaata aagtttctta agattgaatc ctggtgcccg tcttgcatg attatcatat  
846

aatttctggt gaattacggt aagcatgtaa taattaacat gtaatgcatg acgttattta  
906

tgagatgggt ttttatgatt agagtcccgc aattatacat ttaatacgcg atagaaaaca  
966

aaatatagcg cgcaaactag gataaattat cgcgcgcggt gtcactatg ttactagatc  
1026

ggggatcgat  
1036

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<400> 21  
agcttgata aaagagaaa gttgattggc agctgtgttt ggggcgcggt ca  
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<210> 22  
<211> 56  
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<400> 22  
agtgtagttg acggcgcccc aaacacagct gccaatcaac ttgtctcttt tatcca  
56

<210> 23  
<211> 52  
<212> ADN  
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<400> 23  
actacactag tgactgcaac ggcgagtgca agcgcgcggt ttacaagggt gg  
52

<210> 24  
<211> 52

<212> ADN  
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<400> 24  
cacaatggcc acccttgtaa ccgcgggcgct tgcactcgcc gttgcagtca ct  
52

<210> 25  
<211> 56  
<212> ADN  
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<400> 25  
ccattgtgga tccttcgcta acgttaactg ttgggtgtaa acctgatagg tcgaca  
56

<210> 26  
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<212> ADN  
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<400> 26  
gatctgtcga cctatcaggt ttcacaccaa cagttaacgt tagcgaagga tc  
52

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<400> 27  
gaccttcgc taacgttaac tgttggtgta gaacctgata gg  
42

<210> 28  
<211> 42  
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<400> 28  
tcgacctatc aggttctaca ccaacagtta acgttagcga ag  
42

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<400> 29  
ctagtgactg caacggcgag tgcttggtgc gc  
32

<210> 30  
<211> 26  
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<400> 30  
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26

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32

<210> 32  
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<400> 32  
gccgcttgca ctcagcagcg cagtca  
26

<210> 33  
<211> 40  
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<400> 33  
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40

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<400> 34  
ggggcgccgt caactaca  
18

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ctagtgtagt tgacggcgcc cc  
22

<210> 36  
<211> 36  
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aaacacagct accagcagca gcagctcttt tatcca  
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<400> 37  
ctagtgactg cgctgctgag tgcttgttgc gc  
32

<210> 38  
<211> 26  
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<400> 38

gcaacaagca ctcagcagcg cagtca  
26